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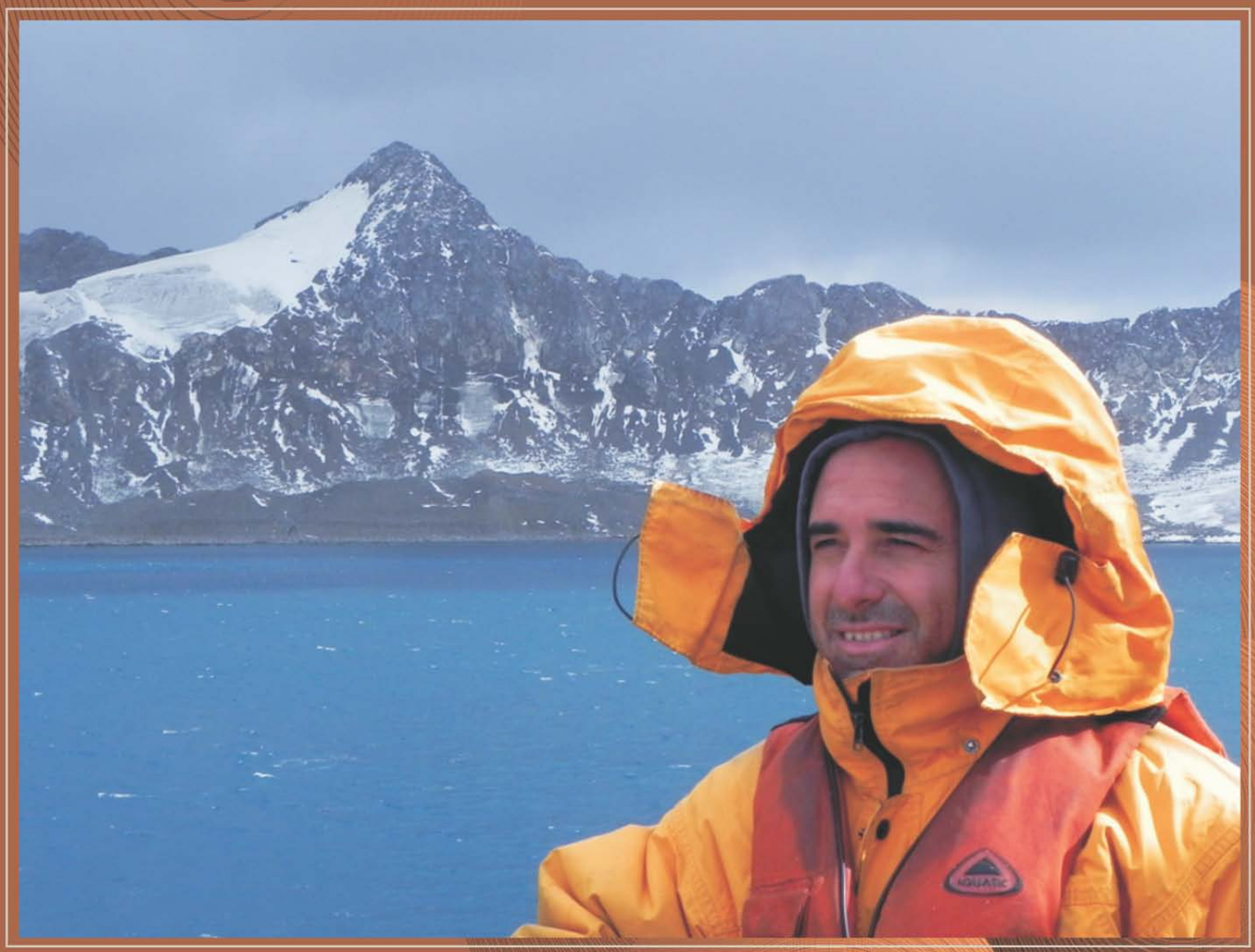
Semblanzas Ictiológicas
Ezequiel Mabragaña



Hugo L. López
y
Justina Ponte Gómez

Indizada en la base de datos ASFA C.S.A.
2013

Semblanzas Ictiológicas

Ezequiel Mabragaña

Tocando el bajo en su casamiento, 9 de abril de 2011

Hugo L. López y Justina Ponte Gómez

ProBiota
División Zoología Vertebrados
Museo de La Plata
FCNyM, UNLP

Diciembre, 2013

Imagen de Tapa
Ezequiel Mabragaña en el buque Puerto Deseado, Antártida

El tiempo acaso no exista. Es posible que no pase y sólo pasemos nosotros.

Tulio Carella

Cinco minutos bastan para soñar toda una vida, así de relativo es el tiempo.

Mario Benedetti

Semblanzas Ictiológicas

A través de esta serie intentaremos conocer diferentes facetas personales de los integrantes de nuestra "comunidad".

El cuestionario, además de su principal objetivo, con sus respuestas quizás nos ayude a encontrar entre nosotros puntos en común que vayan más allá de nuestros temas de trabajo y sea un aporte a futuros estudios históricos.

Esperamos que esta iniciativa pueda ser otro nexo entre los ictiólogos de la región, ya que consideramos que el resultado general trascendería nuestras fronteras.

Hugo L. López

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Lugar de nacimiento: Capital Federal
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Título máximo, Facultad y Universidad: Doctor en Ciencias Biológicas, Facultad de Ciencias Exactas y Naturales, Universidad Nacional de Mar del Plata (UNMdP)
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Especialidad o línea de trabajo: Taxonomía y Bioecología de Peces, en particular rayas (Chondrichthyes, Rajidae)
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Cuestonario

-**Un libro**: *Alexandros* de Valerio Máximo Manfredi

-**Una película**: *El abogado del diablo*

-**Un CD** : Eric Clapton - Unplugged

-**Un artista**: Miguel Angel

-**Un deporte**: fútbol

-**Un color**: azul

-**Una comida**: milanesa a la napolitana con papas fritas

-**Un animal**: guepardo

-**Una palabra**: aventura

-**Un número**: 8

-**Una imagen**: atardecer

-**Un lugar**: Ilha Grande

-**Una estación del año**: primavera

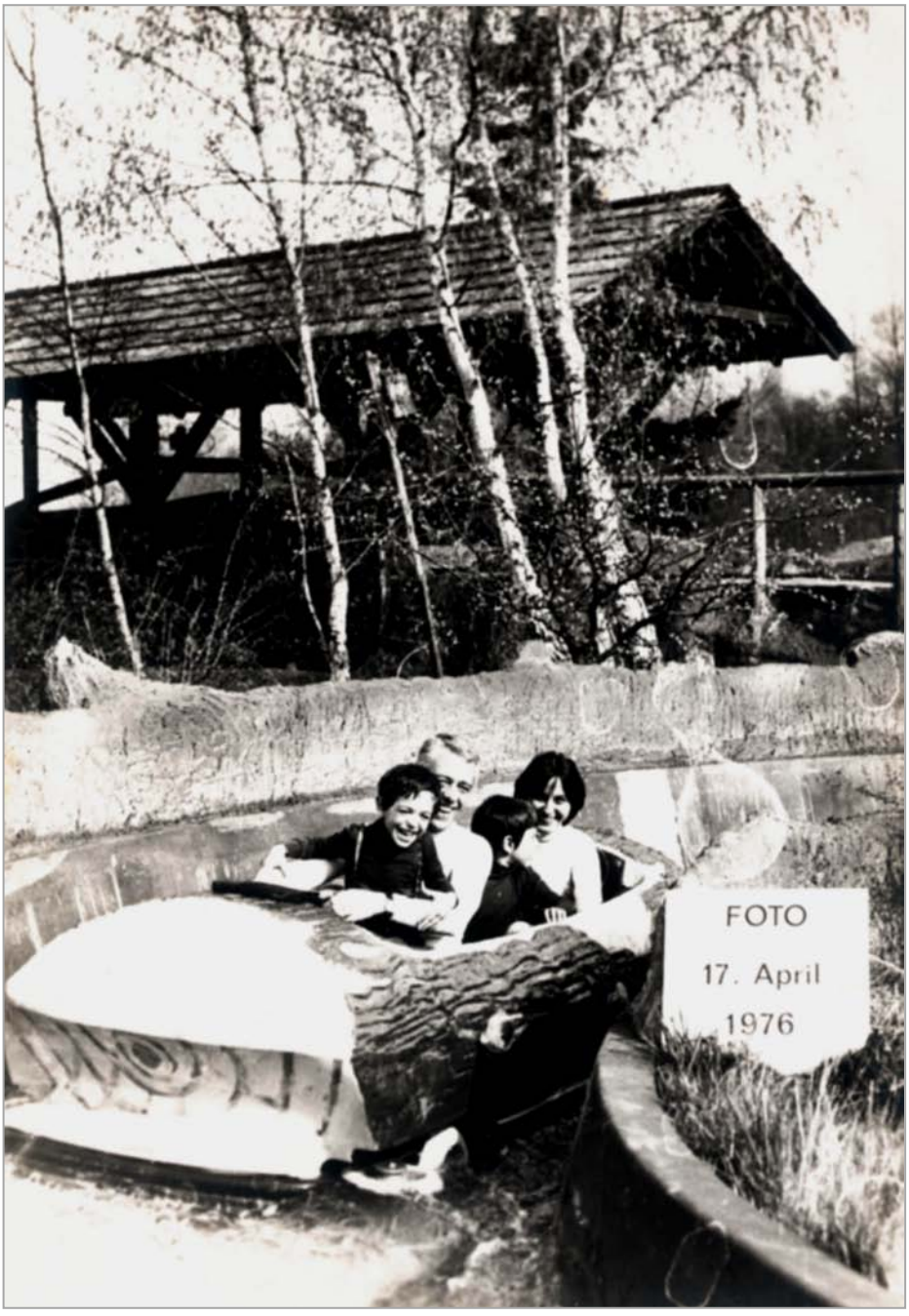
-**Un nombre**: Catalina

-**Un hombre**: Karol Wojtyła

-**Una mujer**: Scarlett Johansson

-**Un personaje de ficción**: La Pantera Rosa

-Un **superhéroe**: Hancock



Ezequiel junto a sus padres y hermano, Bruselas, 1976

Vacaciones en Pinamar, mediados de la década de los 80
Ezequiel, primero a la derecha, con su madre y hermanos

Primer embarque; observador científico a bordo, 1998

Ezequiel Mabragaña junto a su esposa Mariángeles, 9 de abil de 2011

Journal of Fish Biology (2004) **65**, 559–573
doi:10.1111/j.1095-8649.2004.00473.x, available online at http://www.blackwell-synergy.com

Reproductive biology of two sympatric skates in the south-west Atlantic: *Psammobatis rudis* and *Psammobatis normani*

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The total lengths (L_T) at which 50% were mature of *Psammobatis rudis* and *Psammobatis normani*, in the south-west Atlantic were: *P. rudis*, 428 mm for males and 414 mm for females and *P. normani*, 443 mm for males and 403 mm for females. Clasper length in mature males was greater in *P. normani* than in *P. rudis*, whereas oviducal gland width was not different between species. Females of *P. normani* with egg cases were found in every month sampled, and in January, March, April and July in *P. rudis*, although insufficient samples were available to identify peak oviposition times. Geographic variation in size frequency and maturity were found. The effects of oceanographic conditions and fishing pressure are discussed. Size at 50% maturity in both species was >74% of the maximum L_T, indicating late sexual maturity and low potential stock recovery rate.

Key words: maturity; *Psammobatis*; Rajidae; reproduction; south-west Atlantic.

INTRODUCTION

Skates (Rajidae) are becoming increasingly important in south-west Atlantic fisheries (Agnew *et al.*, 1998; Paesch & Meneses, 1999; Cousseau *et al.*, 2000). The low fecundity and late maturity, that is typical of rajid species, indicates that they are particularly vulnerable to fishing pressure and over-exploitation (Walker & Hislop, 1998). Although reproduction is a critical aspect to consider for the success of fisheries management (Pratt & Otake, 1990), little is known about rajid reproduction, and most aspects of their reproductive biology are unknown (Walmsley-Hart *et al.*, 1999). Previous studies on reproduction have focused mainly on north hemisphere species (McEachran, 1970; Du Buit, 1976; Nottage & Perkins, 1983; Luer & Gilbert, 1985; Berestovskii, 1994; Koob *et al.*, 1998; Hamlett, 1999; Hamlett & Koob, 1999).

Demersal fisheries in Argentina take considerable by-catches of skates, which were mostly discarded until the early 1990s. This situation has changed in recent years, and catches increased from 300 t in 1991 to 14 856 t in 1998 (Cousseau *et al.*,

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PLOS one

DNA Barcoding Identifies Argentine Fishes from Marine and Brackish Waters

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Abstract

Background: DNA barcoding has been advanced as a promising tool to aid species identification and discovery through the use of short, standardized gene targets. Despite extensive taxonomic studies, for a variety of reasons the identification of fishes can be problematic, even for experts. DNA barcoding is proving to be a useful tool in this context. However, its broad application is impeded by the need to construct a comprehensive reference sequence library for all fish species. Here, we make a regional contribution to this grand challenge by calibrating the species discrimination efficiency of barcoding among 125 Argentine fish species, representing nearly one third of the known fauna, and examine the utility of these data to address several key taxonomic uncertainties pertaining to species in this region.

Methodology/Principal Findings: Specimens were collected and morphologically identified during cruises conducted between 2005 and 2008. The standard BARCODE fragment of COI was amplified and bi-directionally sequenced from 577 specimens (mean of 5 specimens/species), and all specimens and sequence data were archived and interrogated using analytical tools available on the Barcode of Life Data System (BOLD: www.boldsystems.org). Mostly all species exhibited discrete clusters of closely related haplogroups which permitted the discrimination of 99% of the species (i.e. 119/120) examined while cases of shared haplotypes were detected among just three species-pairs. Notably, barcoding aided the identification of a new species of skate, *Dipturus argentinensis*, permitted the recognition of *Genypterus brachiatus* as a valid species and questions the generic assignment of *Parabathylagus riasolidus*.

Conclusions/Significance: This study constitutes a significant contribution to the global barcode reference sequence library for fishes and demonstrates the utility of barcoding for regional species identification. As an independent assessment of alpha taxonomy, barcodes provide robust support for most morphologically based taxon concepts and also highlight key areas of taxonomic uncertainty worthy of reappraisal.

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Introduction

Despite ongoing scientific debate concerning the role of molecular methods in taxonomy, DNA barcoding has emerged as a widely accepted tool for species identification because of its enhanced focus on standardization and data validation [1]. Barcoding [2–8] seeks to extend species identification capabilities by using short, standardized gene regions for the efficient and cost-effective identification of eukaryotes. Advocating the use of an easily characterized 648 bP fragment from the mitochondrial 5' region of the cytochrome c oxidase subunit I (COI) gene for animal identification, the primary goal of barcoding focuses on the assembly of reference sequence libraries derived from expert-identified voucher specimens in order to develop reliable molecular tools for species identification in nature [3]. Barcoding has been mischaracterized as molecular taxonomy [8], although it is not intended to replace classical taxonomy [1]. Its purpose is to facilitate species identifications by non-experts and to do so in a rapid and cost-effective manner [7]. The effectiveness of barcoding has been demonstrated in diverse taxa, including springtails [8], spiders [9], butterflies [2,3,10–12], flies [13], beetles [14], fishes [15], birds [16,17] and mammals [18–20], with barcoding systems also now being established for plants [21], macroalgae [22], and bacteria [23].

The Fish Barcode of Life campaign (FISH-BOL) [24] seeks to establish a standard reference sequence library for the molecular identification of fishes worldwide [25]. The identification process using COI sequence data for fishes is promising, as supported by recent examples of its applications. DNA barcoding surveys of 207 Australian marine fish species [26] and 260 Australasian shark and ray species [26] have concluded that DNA barcoding can be used

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DNA barcoding Neotropical fishes: recent advances from the Pampa Plain, Argentina

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Abstract

The fish fauna of the Pampa Plain, the southernmost distribution range of many Neotropical species, was barcoded in this study. COI sequences were analysed by means of distance (K2P/NJ) and character-based (ML) models, as well as the Barcode Index Number (BIN). K2P/NJ analysis was able to discriminate among all previously identified species while also revealing the likely occurrence of two cryptic species that were further supported by BIN and ML analyses. On the other hand, both BIN and ML were not able to discriminate between two species of *Rineloricaria*. Despite the small genetic divergence between *A.* cf. *pampa* and *A. eigenmanniorum*, a tight array of haplotypes was observed for each species in both the distance and character-based methods. Deep intraspecific divergences were detected in *Cnesterodon decemmaculatus* (5%) and *Salminus brasiliensis* (6%). For *Salminus brasiliensis*, these findings were further supported by character-based (ML) evidence and meristic and morphological data. Our results also showed that Pampa Plain representatives of *Salminus brasiliensis*, *Rhamdia quelen*, *Hoplias malabaricus*, *Synbranchus marmoratus*, *Australoheros facetus*, *Oligosarcus jenynsii* and *Corydoras paleatus* differed by more than 3% from their conspecifics from other parts of South America. Overall, this study was able to highlight the likely occurrence of a cryptic species in *Salminus brasiliensis* and also illustrate the strong geographical structure in the COI sequence composition of seven fish species from South America.

Keywords: Argentina, biodiversity assessment, DNA barcoding, fish species, *Salminus brasiliensis*

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Introduction

Over the last 250 years, the number of known animal species increased from 4400 to approximately 1.5 million (Chivian & Bernstein 2008). The most conservative estimations suggest that we have discovered only 10% of the animal species present in our planet (Mora *et al.* 2011). At this rate, life may not be completely inventoried for several millennia (Packer *et al.* 2009). For the past 45 years, approximately 300 new species of fishes have been described each year, increasing the number of known species from 18 818 in the 1970s (Nelson 1976) to more than 32 000 today (Eschmeyer 2012). This number represents slightly more than half of all vertebrates on Earth (Nelson 2006).

Neotropical fishes are approximately 15% of all vertebrate biodiversity, occurring in <0.003% of the world's water (Vari & Malabarba 1998). About 4500 fish species have already been described in the Neotropics, but the total number is speculated to rise to 6000 or even 8000 species (Reis *et al.* 2003). Indeed, many emblematic species of this continent, such as *Hoplias malabaricus*, *Eigenmannia virescens* and *Synbranchus marmoratus*, are well-known species complexes (Reis *et al.* 2003; de Carvalho *et al.* 2011), further enhancing the intricacy and controversial taxonomy of many Neotropical fishes. Therefore, it seems mandatory to accelerate and simplify the processes involved in the identification of these species.

Historically, the taxonomic description of species was largely based on morphological characters. However, phenotypic plasticity and genotypic variation in the features used in descriptions can lead to misdiagnoses. Furthermore, cryptic species or differing life stages may add to the confusion. One decade ago, the DNA sequencing technology introduced the possibility of using variation in short sequences of mitochondrial DNA as labels for specimens in a process known as DNA barcoding (Hebert *et al.*

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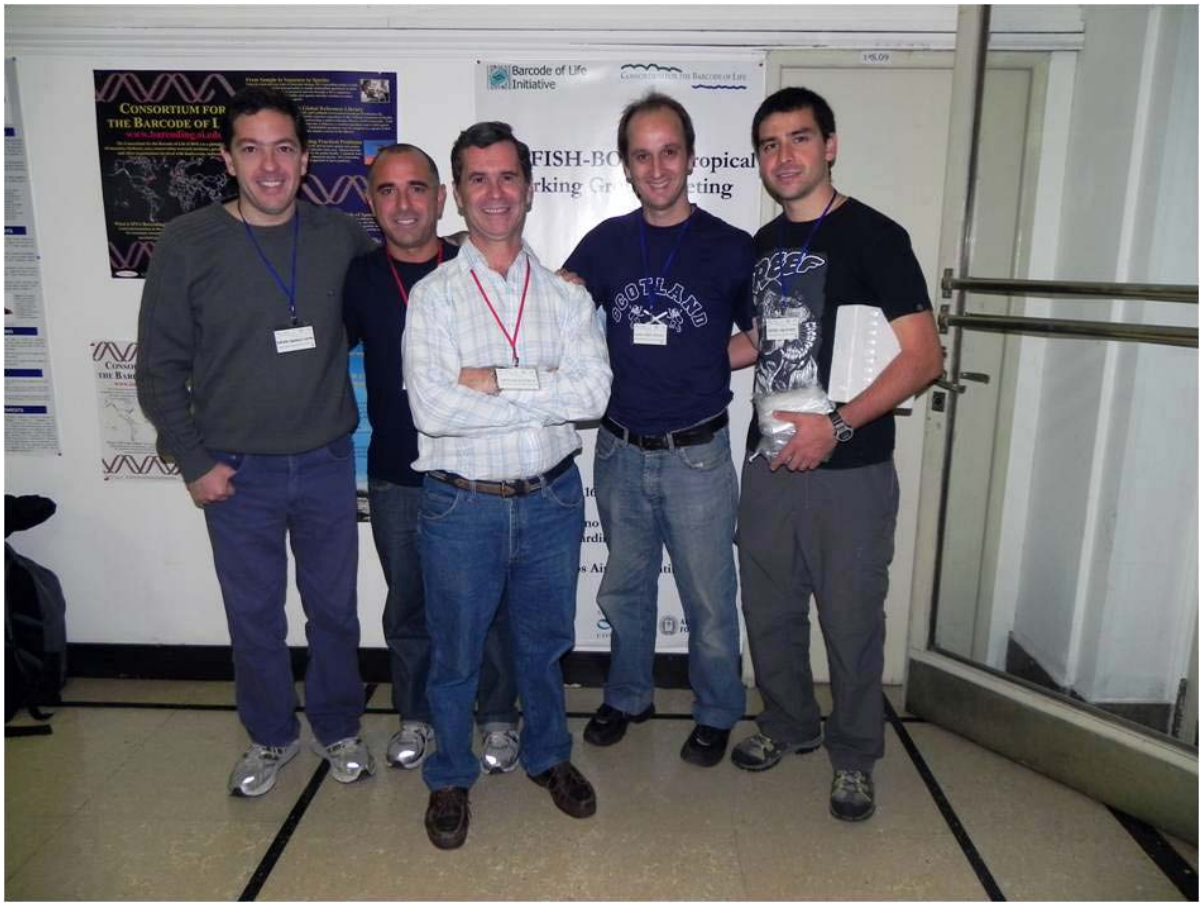

Taller de BARCODE con el grupo Biotaxonomía Morfológica y Molecular de Peces (BIMOPE), Ciudad Autónoma de Buenos Aires, mayo 2010
Adelante: Juan Martín Díaz de Astarloa; atrás de izquierda a derecha: Mariano González Castro, Ezequiel Mabragaña, Juan José Rosso y Matías Delpiani

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